

SEQUENCE LISTING

<110> BUNEMANN, MORITZ
VILARDAGA, JEAN PIERRE
HOFFMAN, CARSTEN
LOHSE, MARTIN JOHANNES

<120> MILLISECOND ACTIVATION SWITCH FOR SEVEN-TRANSMEMBRANE PROTEINS

<130> VOSS:008US

<140> 10/538985

<141> 2005-06-15

<150> DE 102 59 874.6

<151> 2002-12-19

<150> DE 102 59 874.6

<151> 2002-12-19

<150> EP 03 00 4394.7

<151> 2003-03-03

<160> 46

<170> PatentIn version 3.1

<210> 1

<211> 1409

<212> DNA

<213> Mouse

<400> 1

atgggctacc catacgacgt cccagactac gccagcatgg gctcactgca gccggatgcc	60
ggcaacagca gctggaacgg gaccgaagcg cccggaggcg gcacccgagc cacccttac	120
tccctgcagg tgacactgac gctgggtttgc ctggctggcc tgctcatgct gttcacagta	180
tttggaacg tgctggttat tatcgcggtg ttcaccagtc gcgcgctcaa agtccccaa	240
aacctcttcc tgggtgtccct ggctcagcg gacatcctgg tggccacgct ggtcattccc	300
ttttctttg ccaacgaggt tatgggttac tggactttg gtaaggtgtg gtgtgagatc	360

tatttggtc	tcgacgtgct	cttttgcacg	tcgtccatag	tgcacctgtg	cgccatcagc	420
cttgaccgct	actggtccat	cacgcaggcc	atcgagtaca	acctgaagcg	cacgccgcgt	480
cgcacaaagg	ccatcattgt	caccgtgtgg	gtcatctcgg	ctgtcatctc	cttcccccca	540
ctcatctcca	tagagaagaa	gaccagaagt	ggatgtgcat	ctcctcgtcc	atcggttcct	600
tcttcgcgcc	ttgcctcatc	atgatcctgg	tctacgtgcg	tatttaccag	atcgccaagc	660
gtcgcacccg	cgtgcctccc	agccgccggg	gtccggacgc	ctgttcgcgc	ccgccggggg	720
gcgccgatcg	caggcccaac	gggctggggc	cggagcgcg	cgcgggtccc	acgggcgctg	780
aggcggagcc	gctgcccacc	cagcttaacg	gtgccccggg	ggagcccgcg	cccgccgggc	840
cccgcgatgg	ggatgcgctg	gacctagagg	agagttcgtc	gtccgagcac	gccgagcggc	900
ccccggggcc	ccgcagaccc	gaccgcggcc	cccagaccaa	gggcaagacc	cgggcgagtc	960
aggtgaagcc	gggggacagt	ctgccgcggc	gcggggcccg	ggccgcgggg	ccgggggctt	1020
cgggggtccg	gcacggagag	gagcgcgcg	ggggcgccaa	agcgtcgcgc	tggcgcgggg	1080
ggcaaaaccg	ggagaaacgc	ttcacgttcg	tgctggcggg	ggtgatcggc	gtgttcgtgg	1140
tgtgttggtt	tccgttcttt	ttcacctaca	cgctcatagc	ggtcggctgc	ccggtgccca	1200
gccagctctt	caacttcttc	ttctggttcg	gctactgcaa	cagctcgtcg	aaccctgtta	1260
tctacaccat	cttcaaccac	gacttccgac	gcgccttcaa	gaagatcctc	tgccgtgggg	1320
acagaaaacg	catcgtgtga	ttcaaccacg	acttccgacg	cgccttcaag	aagatcctct	1380
gccgtgggga	cagaaaacgc	atcgtgtga				1409

<210> 2

<211> 462

<212> PRT

<213> Mouse

<400> 2

Met	Gly	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	Met	Gly	Ser	Leu
1				5				10					15		

Gln	Pro	Asp	Ala	Gly	Asn	Ser	Ser	Trp	Asn	Gly	Thr	Glu	Ala	Pro	Gly
			20					25					30		

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
 35 40 45

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
 50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
 65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr
 85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
 100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
 115 120 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
 130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
 145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
 165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
 180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
 195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
 210 215 220

Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
 225 230 235 240

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly
 245 250 255

Gly Ala Asp Arg Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly

260	265	270
Pro Thr Gly Ala Glu Ala Glu	Pro Leu Pro Thr Gln Leu Asn Gly Ala	
275	280	285
Pro Gly Glu Pro Ala Pro Ala Gly	Pro Arg Asp Gly Asp Ala Leu Asp	
290	295	300
Leu Glu Glu Ser Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro		
305	310	315
Arg Arg Pro Asp Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser		
	325	330
Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala		
	340	345
Gly Pro Gly Ala Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly		
	355	360
Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe		
	370	375
Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe		
385	390	395
Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val Gly Cys Pro Val Pro		
	405	410
Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser		
	420	425
Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala		
	435	440
Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val		
	450	455

<210> 3

<211> 1785

<212> DNA

<213> homo sapiens

<400> 3

atggggaccg cccggatcgc acccggcctg gcgctcctgc tctgctgccc cgtgctcagc	60
tccgcgtacg cgctggtgga tgcagatgac gtcattgacta aagaggaaca gatcttctctg	120
ctgcaccgtg ctgaggccca gtgcgaaaaa cggctcaagg aggtcctgca gaggccagcc	180
agcataatgg aatcagacaa gggatggaca tctgcgtcca catcaggga gcccaggaaa	240
gataaggcat ctgggaagct ctaccctgag tctgaggagg acaaggaggc acccactggc	300
agcaggtacc gagggcgccc ctgtctgccc gaatgggacc acatcctgtg ctggccgctg	360
ggggcaccag gtgaggtggt ggctgtgccc tgtccggact acatttatga cttcaatcac	420
aaaggccatg cctaccgacg ctgtgaccgc aatggcagct gggagctggt gcctgggcac	480
aacaggacgt gggccaacta cagcgagtgt gtcaaatttc tcaccaatga gactcgtgaa	540
cgggaggtgt ttgaccgcct gggcatgatt tacaccgtgg gctactccgt gtccctggcg	600
tccctcaccg tagctgtgct catcctggcc tactttaggc ggctgcactg caccgcgaac	660
tacatccaca tgcacctgtt cctgtccttc atgctgcgcg ccgtgagcat cttcgtcaag	720
gacgctgtgc tctactctgg cgccacgctt gatgaggctg agcgccctac cgaggaggag	780
ctgcgcgcca tcgcccaggc gccccgcgcg cctgccaccg ccgctgcccg ctacgcgggc	840
tgcaggggtg ctgtgacctt ctctctttac ttcttgccca ccaactacta ctggattctg	900
gtggaggggc tgtacctgca cagcctcatc ttcatggcct tcttctcaga gaagaagtac	960
ctgtggggct tcacagtctt cggctgggggt ctgcccgcctg tcttcgtggc tgtgtgggtc	1020
agtgtcagag ctaccctggc caacaccggg tgctgggact tgagctccgg gaacaaaaag	1080
tggatcatcc aggtgcccac cctggcctcc attgtgtcga acttcatect cttcatcaat	1140
atcgtccggg tgctcgccac caagctgcgg gagaccaacg ccggccggtg tgacacacgg	1200
cagcagtacc ggaagctgct caaatccacg ctggtgctca tgcccctctt tggcgtccac	1260
tacattgtct tcatggccac accatacacc gaggtctcag ggacgctctg gcaagtccag	1320
atgcactatg agatgctctt caactccttc cagggatttt ttgtcgcaat catatactgt	1380
ttctgcaatg gcgaggtaca agctgagatc aagaaatctt ggagccgctg gacactggca	1440
ctggacttca agcgaaaggc acgcagcggg agcagcagct atagctacgg ccccatgggtg	1500
tcccacacaa gtgtgaccaa tgtcggcccc cgtgtgggac tcggcctgcc cctcagcccc	1560

cgcctactgc ccactgccac caccaacggc caccctcagc tgctggcca tgccaagcca 1620
 gggaccccag ccctggagac cctcgagacc acaccacctg ccatggctgc tccaaggac 1680
 gatgggttcc tcaacggctc ctgctcaggc ctggacgagg aggcctctgg gcctgagcgg 1740
 ccacctgccc tgctacagga agagtgggag acagtcatgt gatga 1785

<210> 4

<211> 593

<212> PRT

<213> homo sapiens

<400> 4

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met
 20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
 35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
 50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
 65 70 75 80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
 85 90 95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
 100 105 110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
 115 120 125

Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
 130 135 140

Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
145 150 155 160

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
165 170 175

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
180 185 190

Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
195 200 205

Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
210 215 220

His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
225 230 235 240

Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
245 250 255

Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
260 265 270

Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
275 280 285

Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
290 295 300

Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
305 310 315 320

Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val
325 330 335

Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
340 345 350

Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
355 360 365

Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val

370

375

380

Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
 385 390 395 400

Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu
 405 410 415

Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val
 420 425 430

Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn
 435 440 445

Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
 450 455 460

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 465 470 475 480

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 485 490 495

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 500 505 510

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 515 520 525

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 530 535 540

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
 545 550 555 560

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
 565 570 575

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
 580 585 590

Met

<210> 5

<211> 1238

<212> DNA

<213> homo sapiens

<400> 5

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc	60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc	120
accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc aacacatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcctggctct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cgggtacaatg gcttgggtgac cggcacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctaggttgg acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc	540
aacttctttc ctgtgtgctg gtgcccctgc tgcctatgct ggggtgtctat ttgcggatct	600
tcctggcggc gcgacgacag ctgaagcaga tggagagcca gcctctgccg ggggagcggg	660
cacggtccac actgcagaag gaggtccatg ctgccaaagc actggccatc attgtggggc	720
tctttgccct ctgctggctg cccctacaca tcatcaactg cttcactttc ttctgccccg	780
actgcagcca cggccctctc tggtcatgt acctggccat cgtcctctcc cacaccaatt	840
cggttgtgaa tcccttcac taccgctacc gtatccgga gttccgccag acctccgca	900
agatcattcg cagccacgtc ctgaggcagc aagaaccttt caaggcagct ggcaccagt	960
cccgggtctt ggcagctcat ggcagtgcg gagagcaggt cagcctccgt ctcaacggcc	1020
acccgccagg agtgtgggcc aacggcagtg ctccccaccc tgagcggagg cccaatggct	1080
atgcctggg gctggtgagt ggagggagt cccaagagtc ccaggggaac acgggcctcc	1140
cagacgtgga gctccttagc catgagctca agggagtgtg ccagagccc cctggcctag	1200
atgacccctt ggcccaggat ggagcaggag tgtcctga	1238

<210> 6

<211> 391

<212> PRT

<213> homo sapiens

<400> 6

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala
35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr
50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala
65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala
85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn
100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp
115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn
130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu
145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met
165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met

180	185	190
Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys		
195	200	205
Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu		
210	215	220
Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly Leu		
225	230	235
Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr Phe		
245	250	255
Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu Ala		
260	265	270
Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr Ala		
275	280	285
Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser		
290	295	300
His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala		
305	310	315
Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg		
325	330	335
Leu Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His		
340	345	350
Pro Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly		
355	360	365
Ser Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu		
370	375	380
Leu Ser His Glu Leu Lys Gly		
385	390	

<211> 720

<212> DNA

<213> artificial sequence

<220>

<223> eCFP (enhanced CFP) cDNA sequence

<400> 7

```
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac      60
ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac      120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc      180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag      240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc      300
ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg      360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac      420
aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac      480
ggcatcaagg ccaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc      540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac      600
tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc      660
ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagtaa      720
```

<210> 8

<211> 239

<212> PRT

<213> artificial sequence

<220>

<223> eCFP (enhanced CFP) amino acid sequence

<400> 8

```
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1           5           10          15
```

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 9
<211> 720
<212> DNA
<213> artificial sequence

<220>

<223> YFP cDNA sequence

<400> 9
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60
ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ctttcggcta cggcctgcag tgcttcgccc gctaccccga ccacatgaag 240
cagcagcact ttttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600
tacctgagct accagtccgc cctgagcaaa gacccaacg agaagcgcgga tcacatggtc 660
ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagtaa 720

<210> 10
<211> 239
<212> PRT
<213> artificial sequence

<220>

<223> YFP amino acid sequence

<400> 10

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	145	150	155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165	170	175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu	195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	225	230	235

<210> 11

<211> 2457

<212> DNA

<213> artificial sequence

<220>

<223> alpha2a adrenergic receptor-cam cDNA sequence

<400> 11

atgggctacc catacgacgt cccagactac gccagcatgg gctcactgca gccggatgcc	60
ggcaacagca gctggaacgg gaccgaagcg cccggaggcg gcacccgagc cacccttac	120
tccctgcagg tgacactgac gctggtttgc ctggctggcc tgctcatgct gttcacagta	180
tttggaacg tgctggttat tatcgcggtg ttcaccagtc gcgcgctcaa agctcccaa	240
aacctcttcc tgggtgtcct ggctcagcg gacatcctgg tggccacgct ggtcattccc	300
ttttctttgg ccaacgaggt tatgggttac tggtaacttg gtaagggtgtg gtgtgagatc	360
tatttggtc tcgacgtgct cttttgcacg tcgtccatag tgcacctgtg cgccatcagc	420
cttgaccgct actggtccat cacgcaggcc atcgagtaca acctgaagcg cagccgcgt	480
cgcacaaagg ccatcattgt caccgtgtgg gtcattctcg ctgtcatctc cttcccgcca	540
ctcatctcca tagagaagaa gggcgctggc ggcgggcagc agccggccga gccaaagtgc	600
aagatcaacg accagaagtg gtatgtcatc tcctcgtcca tcggttcctt cttecgcgct	660
tgctcatca tgatcctggt ctacgtgctg atttaccaga tcgccaagcg tcgcaccgcg	720
gtgcctccca gccgccgggg tccggacgcc atggtgagca agggcgagga gctgttcacc	780
ggggtggtgc ccatcctggt cgagctggac ggcgacgtaa acggccacaa gttcagcgtg	840
tccggcgagg gcgagggcga tgccacctac ggcaagctga ccctgaagtt catctgcacc	900
accggcaagc tgcccgtgcc ctggcccacc ctctgacca ccttcggcta cggcctgcag	960
tgcttcgccc gctaccccga ccacatgaag cagcacgact tcttcaagtc cgccatgccc	1020
gaaggctacg tccaggagcg caccatcttc ttcaaggacg acggcaacta caagaccgcg	1080
gccgaggtga agttcgaggg cgacaccctg gtgaaccgca tcgagctgaa gggcatcgac	1140
ttcaaggagg acggcaacat cctggggcac aagctggagt acaactaaa cagccacaac	1200

gtctatatca tggccgacaa gcagaagaac ggcatacaagg tgaacttcaa gatccgccac	1260
aacatcgagg acggcagcgt gcagctcgcc gaccactacc agcagaacac ccccatcggc	1320
gacggccccg tgctgctgcc cgacaaccac tacctgagct accagtccgc cctgagcaaa	1380
gaccccaacg agaagcgcgga tcacatggtc ctgctggagt tcgtgaccgc cgccgggatac	1440
actctcggca tggacgagct gtacaagcgc tggcgcgggga ggcaaaaccg ggagaaacgc	1500
ttcacgttcg tgctggcggt ggtgatcggc gtgttcgtgg tgtgttggtt tccgttcttt	1560
ttcacctaca cgctcatagc ggtcggtgc ccggtgccca gccagctctt caacttcttc	1620
ttctgggttcg gctactgcaa cagctcgctg aacctgtta tctacaccat cttcaaccac	1680
gacttccgac gcgccttcaa gaagatcctc tgccgtgggg acagaaaacg catcgtgatg	1740
gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctggtcga gctggacggc	1800
gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc	1860
aagctgacct tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc	1920
gtgaccacct tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag	1980
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgcac catcttcttc	2040
aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg	2100
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag	2160
ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc	2220
atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac	2280
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgccga caaccactac	2340
ctgagcacct agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg	2400
ctggagttcg tgaccgccgc cgggatcact ctcgcatgg acgagctgta caagtaa	2457

<210> 12

<211> 818

<212> PRT

<213> artificial sequence

<220>

<223> alpha 2a adrenergic receptor-cam "chameleon" amino acid sequence

<400> 12

Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Met Gly Ser Leu
1 5 10 15

Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly
20 25 30

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
35 40 45

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr
85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
115 120 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
210 215 220

Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
225 230 235 240

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Met Val Ser Lys Gly Glu
245 250 255

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
260 265 270

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
275 280 285

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
290 295 300

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln
305 310 315 320

Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
325 330 335

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
340 345 350

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
355 360 365

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
370 375 380

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
385 390 395 400

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
405 410 415

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
420 425 430

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
435 440 445

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
450 455 460

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
465 470 475 480

Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Trp Arg Gly Arg Gln Asn
485 490 495

Arg Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe
500 505 510

Val Val Cys Trp Phe Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val
515 520 525

Gly Cys Pro Val Pro Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly
530 535 540

Tyr Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His
545 550 555 560

Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys
565 570 575

Arg Ile Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
580 585 590

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
595 600 605

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
610 615 620

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
625 630 635 640

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
645 650 655

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
660 665 670

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr

675	680	685
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu		
690	695	700
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys		
705	710	715 720
Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys		
	725	730 735
Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu		
	740	745 750
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile		
	755	760 765
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln		
	770	775 780
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu		
785	790	795 800
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu		
	805	810 815

Tyr Lys

<210> 13

<211> 2928

<212> DNA

<213> artificial sequence

<220>

<223> PTH receptor-cam "chameleon" 8 cDNA sequence

<400> 13

atggggaccg cccggatcgc acccggcctg gcgctcctgc tctgctgccc cgtgctcagc	60
tccgcgtacg cgctggtgga tgcagatgac gtcattgacta aagaggaaca gatcttcctg	120

ctgcaccgtg	ctcaggccca	gtgcgaaaaa	cggctcaagg	aggtcctgca	gaggccagcc	180
agcataatgg	aatcagacaa	gggatggaca	tctgcgcca	catcaggga	gccagga	240
gataaggcat	ctgggaagct	ctaccctgag	tctgaggagg	acaaggaggc	accactggc	300
agcaggtacc	gagggcgccc	ctgtctgccc	gaatgggacc	acatcctgtg	ctggccgctg	360
ggggcaccag	gtgaggtggg	ggctgtgccc	tgtccggact	acatttatga	cttcaatcac	420
aaaggccatg	cctaccgacg	ctgtgaccgc	aatggcagct	gggagctggg	gcctgggcac	480
aacaggacgt	gggccaacta	cagcgagtgt	gtcaaatttc	tcaccaatga	gactcgtgaa	540
cgggaggtgt	ttgaccgcct	gggcatgatt	tacaccgtgg	gctactccgt	gtccctggcg	600
tccctcaccg	tagctgtgct	catcctggcc	tactttaggc	ggctgcactg	cacgcgcaac	660
tacatccaca	tgcacctgtt	cctgtccttc	atgctgcgcg	ccgtgagcat	cttcgtcaag	720
gacgctgtgc	tctactctgg	cgccacgctt	gatgaggctg	agcgccctac	cgaggaggag	780
ctgcgcgcca	tcgcccaggc	gccccgcgcg	cctgccaccg	ccgctgccgg	ctacgcgggc	840
tgcaggggtg	ctgtgacctt	cttcctttac	ttcctggcca	ccaactacta	ctggattctg	900
gtggaggggc	tgtacctgca	cagcctcatc	ttcatggcct	tcttctcaga	gaagaagtac	960
ctgtggggct	tcacagtctt	cggctggggg	ctgcccgcctg	tcttcgtggc	tgtgtgggtc	1020
agtgtcagag	ctaccctggc	caacaccggg	tgtggggact	tgagctccgg	gaacaaaaag	1080
tggatcatcc	aggtgcccac	cctggcctcc	attgtgtctca	acttcacctc	cttcatcaat	1140
atcgccggg	tgctcgccac	caagctgcgg	gagaccaacg	ccggcatggg	gagcaagggc	1200
gaggagctgt	tcaccggggg	ggtgcccac	ctggctcgagc	tggacggcga	cgtaaacggc	1260
cacaagttca	gcgtgtccgg	cgagggcgag	ggcgatgcca	cctacggcaa	gctgaccctg	1320
aagttcatct	gcaccaccgg	caagctgccc	gtgccctggc	ccaccctcgt	gaccaccctg	1380
acctggggcg	tgagtgctt	cagccgctac	cccgaccaca	tgaagcagca	cgacttcttc	1440
aagtcgcca	tgcccgaagg	ctacgtccag	gagcgcacca	tcttcttcaa	ggacgacggc	1500
aactacaaga	cccgcgccga	ggtgaagttc	gagggcgaca	ccctggtgaa	ccgcatcgag	1560
ctgaagggca	tcgacttcaa	ggaggacggc	aacatcctgg	ggcacaagct	ggagtacaac	1620
tacatcagcc	acaacgtcta	tatcaccgcc	gacaagcaga	agaacggcat	caaggccaac	1680
ttcaagatcc	gccacaacat	cgaggacggc	agcgtgcagc	tcgccgacca	ctaccagcag	1740
aacaccccca	tcggcgacgg	ccccgtgctg	ctgcccgcga	accactacct	gagcaccag	1800

tccgccctga gcaaagaccc caacgagaag cgcgatcaca tggtcctgct ggagttcgtg	1860
accgccgccg ggatcactct cggcatggac gagctgtaca agcgggtgtga cacacggcag	1920
cagtaccgga agctgctcaa atccacgctg gtgctcatgc ccctctttgg cgtccactac	1980
attgtcttca tggccacacc atacaccgag gtctcagga cgctctggca agtccagatg	2040
cactatgaga tgctcttcaa ctccctccag ggattttttg tcgcaatcat atactgtttc	2100
tgcaatggcg aggtacaagc tgagatcaag aaatcttggg gccgctggac actggcactg	2160
gacttcaagc gaaaggcacg cagcgggagc agcagctata gctacggcat ggtgagcaag	2220
ggcgaggagc tggtcaccgg ggtgggtgcc atcctggtcg agctggacgg cgacgtaaac	2280
ggccacaagt tcagcgtgtc cggcgagggc gagggcgatg ccacctacgg caagctgacc	2340
ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtgaccacc	2400
ttcggctacg gcctgcagtg cttcgcccgc taccctgacc acatgaagca gcacgacttc	2460
ttcaagtccg ccatgcccga aggctacgtc caggagcgca ccatcttctt caaggacgac	2520
ggcaactaca agaccgcgc cgaggtgaag ttcgagggcg acaccctggg gaaccgcatc	2580
gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacia gctggagtac	2640
aactacaaca gccacaacgt ctatatcatg gccgacaagc agaagaacgg catcaagggtg	2700
aacttcaaga tccgccacia catcgaggac ggcagcgtgc agctcgccga ccactaccag	2760
cagaacaccc ccatcgccga cggccccgtg ctgctgcccg acaaccacta cctgagctac	2820
cagtccgcc tgagcaaaga cccaacgag aagcgcgatc acatggtcct gctggagttc	2880
gtgaccgccg ccgggatcac tctcggcatg gacgagctgt acaagtaa	2928

<210> 14

<211> 975

<212> PRT

<213> artificial sequence

<220>

<223> PTH receptor-cam8 "chameleon" amino acid sequence

<400> 14

Met	Gly	Thr	Ala	Arg	Ile	Ala	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Cys	Cys
1				5				10						15	

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met
20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
65 70 75 80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
85 90 95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
100 105 110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
115 120 125

Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
130 135 140

Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
145 150 155 160

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
165 170 175

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
180 185 190

Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
195 200 205

Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
210 215 220

His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
225 230 235 240

Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
245 250 255

Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
260 265 270

Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
275 280 285

Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
290 295 300

Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
305 310 315 320

Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val
325 330 335

Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
340 345 350

Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
355 360 365

Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val
370 375 380

Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Met Val Ser Lys Gly
385 390 395 400

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
405 410 415

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
420 425 430

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
435 440 445

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val
450 455 460

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
465 470 475 480

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
485 490 495

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
500 505 510

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
515 520 525

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
530 535 540

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
545 550 555 560

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
565 570 575

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
580 585 590

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
595 600 605

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
610 615 620

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Cys Asp Thr Arg Gln
625 630 635 640

Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
645 650 655

Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
660 665 670

Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
675 680 685

Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu

690				695				700							
Val 705	Gln	Ala	Glu	Ile	Lys 710	Lys	Ser	Trp	Ser	Arg 715	Trp	Thr	Leu	Ala	Leu 720
Asp	Phe	Lys	Arg	Lys 725	Ala	Arg	Ser	Gly	Ser 730	Ser	Ser	Tyr	Ser	Tyr 735	Gly
Met	Val	Ser	Lys 740	Gly	Glu	Glu	Leu	Phe 745	Thr	Gly	Val	Val	Pro 750	Ile	Leu
Val	Glu	Leu 755	Asp	Gly	Asp	Val	Asn 760	Gly	His	Lys	Phe 765	Ser	Val	Ser	Gly
Glu	Gly 770	Glu	Gly	Asp	Ala	Thr 775	Tyr	Gly	Lys	Leu	Thr 780	Leu	Lys	Phe	Ile
Cys 785	Thr	Thr	Gly	Lys	Leu 790	Pro	Val	Pro	Trp	Pro 795	Thr	Leu	Val	Thr	Thr 800
Phe	Gly	Tyr	Gly	Leu 805	Gln	Cys	Phe	Ala	Arg 810	Tyr	Pro	Asp	His	Met 815	Lys
Gln	His	Asp	Phe 820	Phe	Lys	Ser	Ala	Met 825	Pro	Glu	Gly	Tyr	Val 830	Gln	Glu
Arg	Thr 835	Ile	Phe	Phe	Lys	Asp	Asp 840	Gly	Asn	Tyr	Lys	Thr 845	Arg	Ala	Glu
Val	Lys 850	Phe	Glu	Gly	Asp	Thr 855	Leu	Val	Asn	Arg	Ile 860	Glu	Leu	Lys	Gly
Ile 865	Asp	Phe	Lys	Glu	Asp 870	Gly	Asn	Ile	Leu	Gly 875	His	Lys	Leu	Glu	Tyr 880
Asn	Tyr	Asn	Ser	His 885	Asn	Val	Tyr	Ile	Met 890	Ala	Asp	Lys	Gln	Lys 895	Asn
Gly	Ile	Lys	Val 900	Asn	Phe	Lys	Ile	Arg 905	His	Asn	Ile	Glu	Asp 910	Gly	Ser
Val	Gln	Leu 915	Ala	Asp	His	Tyr	Gln 920	Gln	Asn	Thr	Pro	Ile 925	Gly	Asp	Gly

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 930 935 940

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 945 950 955 960

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 965 970 975

<210> 15

<211> 2361

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP14/10-YFP-C33 cDNA sequence; A2A "chameleon"

<400> 15

atgccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc	60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc	120
accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc aaccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcctggctct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cggcacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtggtccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggaggtga gcaagggcga ggagctgttc	660
accggggtgg tgccatcct ggtcgagctg gacggcgacg taaacggcca caagttcagc	720
gtgtccggcg agggcgaggg cgatgccacc tacggcaagc tgaccctgaa gttcatctgc	780
accaccggca agctgcccgt gccctggccc accctcgtga ccaccctgac ctggggcgctg	840

cagtgttca gccgtaccc cgaccacatg aagcagcacg acttcttcaa gtccgccatg	900
cccgaaggct acgtccagga gcgcaccatc ttcttcaagg acgacggcaa ctacaagacc	960
cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc gcatcgagct gaagggcatc	1020
gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta catcagccac	1080
aacgtctata tcaccgccga caagcagaag aacggcatca aggccaactt caagatccgc	1140
cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa ccccccatc	1200
ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcaccagtc cgccctgagc	1260
aaagacccca acgagaagcg cgatcacatg gtctgtctgg agttcgtgac cgccgcccgg	1320
atcactctcg gcatggacga gctgtacaag cttcagaagg aggtccatgc tgccaagtca	1380
ctggccatca ttgtggggct ctttgccctc tgetggctgc ccctacacat catcaactgc	1440
ttcactttct tctgccccga ctgcagccac gcccctctct ggctcatgta cctggccatc	1500
gtcctctccc acaccaattc ggttgtgaat cccttcatct acgcctaccg tatccgcgag	1560
ttccgccaga ctttcgcaa gatcattcgc agccacgtcc tgaggcagca agaacctttc	1620
aaggcagctg gcaccagtc cggggtcgtg agcaagggcg aggagctgtt caccggggtg	1680
gtgcccaccc tggtcgagct ggacggcgac gtaaaccggc acaagttcag cgtgtccggc	1740
gagggcgagg gcgatgccac ctacggcaag ctgaccctga agttcatctg caccaccggc	1800
aagctgcccg tgccctggcc caccctcgtg accaccttcg gctacggcct gcagtgttc	1860
gcccgtacc ccgaccacat gaagcagcac gacttcttca agtccgccat gcccgaggc	1920
tacgtccagg agcgcacat cttcttcaag gacgacggca actacaagac ccgcgccgag	1980
gtgaagttcg agggcgacac cctggtgaac cgcacgagc tgaagggcat cgacttcaag	2040
gaggacggca acatcctggg gcacaagctg gagtacaact acaacagcca caacgtctat	2100
atcatggccg acaagcagaa gaacggcatc aaggtgaact tcaagatccg ccacaacatc	2160
gaggacggca gcgtgcagct cgccgaccac taccagcaga acaccccat cggcgacggc	2220
cccgtgctgc tgcccgacaa ccactacctg agtaccagt ccgccctgag caaagacccc	2280
aacgagaagc gcgatcacat ggtcctgctg gagttcgtga ccgccgccgg gatcactctc	2340
ggcatggacg agctgtacaa g	2361

<210> 16

<211> 784

<212> PRT

<213> artificial sequence

<220>

<223> A2A-CFP14/10-YFP-C33 amino acid sequence; "A2A chameleon"

<400> 16

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala
35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr
50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala
65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala
85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn
100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp
115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn
130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu
145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met
165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met

180	185	190
Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys		
195	200	205
Gln Met Glu Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
210	215	220
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val		
225	230	235
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
	245	250
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
	260	265
Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His		
	275	280
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
	290	295
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg		
305	310	315
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu		
	325	330
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu		
	340	345
Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln		
	355	360
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
	370	375
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
385	390	395
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
	405	410
		415

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
420 425 430

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
435 440 445

Lys Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val
450 455 460

Gly Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe
465 470 475 480

Thr Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr
485 490 495

Leu Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile
500 505 510

Tyr Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile
515 520 525

Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr
530 535 540

Ser Ala Arg Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
545 550 555 560

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
565 570 575

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
580 585 590

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
595 600 605

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
610 615 620

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
625 630 635 640

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
645 650 655

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
660 665 670

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
675 680 685

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
690 695 700

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
705 710 715 720

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
725 730 735

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
740 745 750

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
755 760 765

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
770 775 780

<210> 17

<211> 477

<212> DNA

<213> Mouse

<400> 17

gtgctgtattt accagatcgc caagcgtcgc acccgcgtgc ctcccagccg ccgggggtccg	60
gacgcctgtt ccgcgccgcc ggggggcgcc gatcgcaggc ccaacgggct gggcccggag	120
cgcggcgcgg gtcccacggg cgctgaggcg gagccgctgc ccacccagct taacgggtgcc	180
ccggggggagc ccgcgcccgc cgggccccgc gatggggatg cgctggacct agaggagagt	240
tcgtcgtccg agcacgccga gcggcccccg gggccccgca gaccgcaccg cggcccccca	300

gccaagggca agaccgggc gagtcaggtg aagccggggg acagtctgcc gcggcgcggg 360
 cccggggccg cggggccggg ggcttcgggg tccgggcacg gagaggagcg cggcgggggc 420
 gccaaagcgt cgcgctggcg cgggaggcaa aaccgggaga aacgcttcac gttcgtg 477

<210> 18

<211> 159

<212> PRT

<213> Mouse

<400> 18

Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg Val Pro Pro Ser
 1 5 10 15

Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly Gly Ala Asp Arg
 20 25 30

Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly Pro Thr Gly Ala
 35 40 45

Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala Pro Gly Glu Pro
 50 55 60

Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp Leu Glu Glu Ser
 65 70 75 80

Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro Arg Arg Pro Asp
 85 90 95

Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser Gln Val Lys Pro
 100 105 110

Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala Gly Pro Gly Ala
 115 120 125

Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly Ala Lys Ala Ser
 130 135 140

Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe Thr Phe Val

155

<213> Mouse

tga	63
-----	----

<213> Mouse

His Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg
1 5 10 15

<213> homo sapiens

<210> 22

<211> 36

<212> PRT

<213> homo sapiens

<400> 22

Arg	Ile	Phe	Leu	Ala	Ala	Arg	Arg	Gln	Leu	Lys	Gln	Met	Glu	Ser	Gln
1				5				10					15		

Pro	Leu	Pro	Gly	Glu	Arg	Ala	Arg	Ser	Thr	Leu	Gln	Lys	Glu	Val	His
			20					25					30		

Ala	Ala	Lys	Ser
			35

<210> 23

<211> 369

<212> DNA

<213> homo sapiens

<400> 23

cgtatccgcg agttccgcc aacattccgc aagatcattc gcagccacgt cctgaggcag	60
caagaacctt tcaaggcagc tggcaccagt gcccggtct tggcagctca tggcagtgac	120
ggagagcagg tcagcctccg tctcaacggc caccgccag gagtgtgggc caacggcagt	180
gctccccacc ctgagcggag gcccaatggc tatgccctgg ggctgggtgag tggagggagt	240
gcccaagagt cccaggggaa cacgggcctc ccagacgtgg agtccttag ccatgagctc	300
aaggagagtgt gccagagcc ccttggccta gatgaccccc tggcccagga tggagcagga	360
gtgtcctga	369

<210> 24

<211> 102

<212> PRT

<213> homo sapiens

<400> 24

Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His
1 5 10 15

Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg
20 25 30

Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg Leu
35 40 45

Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro
50 55 60

Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly Ser
65 70 75 80

Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu Leu
85 90 95

Ser His Glu Leu Lys Gly
100

<210> 25

<211> 57

<212> DNA

<213> homo sapiens

<400> 25

accaagctgc gggagaccaa cgccggccgg tgtgacacac ggcagcagta ccggaag

57

<210> 26

<211> 19

<212> PRT

<213> homo sapiens

<400> 26

Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln
 1 5 10 15

Tyr Arg Lys

<210> 27

<211> 393

<212> DNA

<213> homo sapiens

<400> 27

gaggtacaag ctgagatcaa gaaatcttgg agccgctgga cactggcact ggacttcaag 60
 cgaaaggcac gcagcgggag cagcagctat agctacggcc ccatggtgtc ccacacaagt 120
 gtgaccaatg tcggcccccg tgtgggactc ggcttgcccc tcagcccccg cctactgccc 180
 actgccacca ccaacggcca ccctcagctg cctggccatg ccaagccagg gaccccagcc 240-
 ctggagaccc tcgagaccac accacctgcc atggctgctc ccaaggacga tgggttcctc 300
 aacggctcct gctcaggcct ggacgaggag gcctctgggc ctgagcggcc acctgcctg 360
 ctacaggaag agtgggagac agtcatgtga tga 393

<210> 28

<211> 129

<212> PRT

<213> homo sapiens

<400> 28

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
115 120 125

Met

<210> 29

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam7 amino acid sequence

<400> 29

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Met Val Ser Lys Gly Glu Glu
20 25 30

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
35 40 45

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
50 55 60

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
65 70 75 80

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
85 90 95

Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
100 105 110

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
115 120 125

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
245 250 255

Leu Gly Met Asp Glu Leu Tyr Lys
260

<210> 30

<211> 270

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam9 amino acid sequence

<400> 30

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Met
20 25 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
35 40 45

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
50 55 60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
65 70 75 80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
85 90 95

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
100 105 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
115 120 125

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
130 135 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
145 150 155 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
165 170 175

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly

	180		185		190
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val					
	195		200		205
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro					
	210		215		220
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser					
	225		230		235
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val					
		245		250	255
Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys					
	260		265		270
<210> 31					
<211> 272					
<212> PRT					
<213> artificial sequence					
<220>					
<223> PTHR-cam8 amino acid sequence					
<400> 31					
Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala					
1		5		10	15
Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr					
	20		25		30
Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile					
	35		40		45
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser					
	50		55		60
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe					
65		70		75	80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
85 90 95

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met
100 105 110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
115 120 125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
130 135 140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
145 150 155 160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
165 170 175

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
180 185 190

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
195 200 205

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
210 215 220

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
225 230 235 240

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
245 250 255

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
260 265 270

<210> 32

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam2 amino acid sequence

<400> 32

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
35 40 45

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
50 55 60

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
65 70 75 80

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
85 90 95

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
100 105 110

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
115 120 125

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
130 135 140

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
145 150 155 160

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
165 170 175

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
180 185 190

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
195 200 205

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
210 215 220

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
225 230 235 240

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
245 250 255

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
260 265 270

Leu Tyr Lys
275

<210> 33

<211> 289

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam5 amino acid sequence

<400> 33

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
50 55 60

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
65 70 75 80

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
85 90 95

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
100 105 110

Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His
115 120 125

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
130 135 140

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
145 150 155 160

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
165 170 175

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
180 185 190

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
195 200 205

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
210 215 220

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
225 230 235 240

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
245 250 255

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
260 265 270

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
275 280 285

Lys

<210> 34

<211> 325

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-caml amino acid sequence

<400> ` 34

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr
85 90 95

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
100 105 110

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
115 120 125

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
130 135 140

Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg
145 150 155 160

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
165 170 175

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
180 185 190

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
195 200 205

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
210 215 220

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
225 230 235 240

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
245 250 255

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
260 265 270

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
275 280 285

Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
290 295 300

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
305 310 315 320

Asp Glu Leu Tyr Lys
325

<210> 35

<211> 339

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam4 amino acid sequence

<400> 35

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
100 105 110

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
115 120 125

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
130 135 140

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
145 150 155 160

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
165 170 175

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
180 185 190

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
195 200 205

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
210 215 220

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
225 230 235 240

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
245 250 255

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
260 265 270

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
275 280 285

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
290 295 300

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
305 310 315 320

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
325 330 335

Leu Tyr Lys

<210> 36

<211> 354

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam3 amino acid sequence

<400> 36

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
100 105 110

Gly Pro Glu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
115 120 125

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
130 135 140

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
145 150 155 160

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
165 170 175

Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp
180 185 190

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
195 200 205

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
210 215 220

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
225 230 235 240

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys

Gly	Leu	Gly	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Leu	Pro	Thr	Ala	Thr	Thr	50	55	60	
Asn	Gly	His	Pro	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	Thr	Pro	Ala	65	70	75	80
Leu	Glu	Thr	Leu	Glu	Thr	Thr	Pro	Pro	Ala	Met	Ala	Ala	Pro	Lys	Asp	85	90	95	
Asp	Gly	Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu	Glu	Ala	Ser	100	105	110	
Gly	Pro	Glu	Arg	Pro	Pro	Ala	Leu	Leu	Gln	Glu	Glu	Trp	Glu	Thr	Val	115	120	125	
Met	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	130	135	140	
Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	145	150	155	160
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	165	170	175	
Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	180	185	190	
Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	195	200	205	
Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	210	215	220	
Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	225	230	235	240
Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	245	250	255	
Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	260	265	270	

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
275 280 285

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
290 295 300

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
305 310 315 320

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
325 330 335

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
340 345 350

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
355 360 365

<210> 38

<211> 518

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-PTHR-FRETcontrol amino acid sequence

<400> 38

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Met Val Ser Lys Gly Glu Glu Leu
20 25 30

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
35 40 45

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
50 55 60

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
65 70 75 80

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
85 90 95

Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
100 105 110

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
115 120 125

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
130 135 140

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
145 150 155 160

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
165 170 175

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
180 185 190

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
195 200 205

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
210 215 220

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
225 230 235 240

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
245 250 255

Gly Met Asp Glu Leu Tyr Lys Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
260 265 270

Pro Met Val Ser His Thr Ser Met Val Ser Lys Gly Glu Glu Leu Phe
275 280 285

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly

290		295		300
His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly				
305		310		315 320
Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro				
	325		330	335
Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser				
	340		345	350
Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met				
	355		360	365
Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly				
	370		375	380
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val				
385		390		395 400
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile				
	405		410	415
Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile				
	420		425	430
Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg				
	435		440	445
His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln				
	450		455	460
Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr				
465		470		475 480
Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp				
	485		490	495
His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly				
	500		505	510
Met Asp Glu Leu Tyr Lys				
	515			

<210> 39

<211> 1737

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 cDNA sequence

<400> 39

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc	60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc	120
accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcca tcaccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcttggtcct cagcgagagc tccatcttca gtctcctggc catcgccatt	300
gaccgtaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cgggacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctaggttga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg	480
gagggccaaag tggcctgtct ctttgaggat gtgggtccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt	660
gcacggcca cactgcagaa ggaggtccat gctgccaaagt cactggccat cattgtgggg	720
ctctttgccc tctgctggct gccctacac atcatcaact gcttcacttt cttctgcccc	780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat	840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc	900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt	960
gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggt	1020
gtgagcaagg gcgaggagct gttcaccggg gtgggtgcca tctggtcga gctggacggc	1080
gacgtaaacy gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc	1140
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gccaccctc	1200

gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260
 cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgtac catcttcttc 1320
 aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg 1380
 aaccgcatcg agctgaagg catcgacttc aaggaggacg gcaacatcct ggggcacaag 1440
 ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc 1500
 atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560
 cactaccagc agaacacccc catcgggcgc ggccccgtgc tgctgcccga caaccactac 1620
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680
 ctggagttcg tgaccgccgc cgggatcact ctcgcatgg acgagctgta caagtaa 1737

<210> 40

<211> 578

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 amino acid sequence

<400> 40

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
 35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
565 570 575

Tyr Lys

<210> 41

<211> 1686

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 cDNA sequence

<400> 41

atgccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc	60
atcctgggca atgtgctggt gtgctgggccc gtgtggctca acagcaacct gcagaacgtc	120
accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgccca tcaccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcttggtcct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cgggtacaatg gcttggtgac cgggacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctaggttggga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtgggtccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt	660
gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg	720
ctctttgccc tctgctggtt gccctacac atcatcaact gtttcacttt cttctgcccc	780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat	840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc	900

aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt 960
gcccgggtcg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctgggtcgag 1020
ctggacggcg acgtaaacgg ccacaggttc agcgtgtccg gcgagggcga gggcgatgcc 1080
acctacggca agctgaccct gaagtccatc tgcaccaccg gcaagctgcc cgtgccctgg 1140
cccaccctcg tgaccaccct gacctggggc gtgcagtgtc tcagccgcta ccccgaccac 1200
atgaagcagc acgacttctt caagtccgcc atgccgaag gctacgtcca ggagcgtacc 1260
atcttcttca aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac 1320
accctggtga accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg 1380
gggcacaagc tggagtacaa ctacatcagc cacaacgtct atatcaccgc cgacaagcag 1440
aagaacggca tcaaggccca cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag 1500
ctcgccgacc actaccagca gaacaccccc atcgggcgacg gccccgtgct gctgcccgac 1560
aaccactacc tgagcaccca gtccgccctg agcaaagacc ccaacgagaa gcgcgatcac 1620
atggtcctgc tggagttcgt gaccgcccgc gggatcactc tcggcatgga cgagctgtac 1680
aagtaa 1686

<210> 42

<211> 561

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 amino acid sequence

<400> 42

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr

275		280		285
Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg	290	295	300	
Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser	305	310	315	320
Ala Arg Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro	325	330	335	
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val	340	345	350	
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	355	360	365	
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val	370	375	380	
Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His	385	390	395	400
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val	405	410	415	
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg	420	425	430	
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu	435	440	445	
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu	450	455	460	
Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln	465	470	475	480
Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp	485	490	495	
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	500	505	510	

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
515 520 525

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
530 535 540

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
545 550 555 560

Lys

<210> 43

<211> 1788

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP-ModelPG-C49 cDNA sequence

<400> 43

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc	60
atcctgggca atgtgctggt gtgctgggccc gtgtggctca acagcaacct gcagaacgctc	120
accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc taccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt	240
gcctgcttcg tcttggctct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cggcacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctagggttga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agcctctgcc gggggagcgg	660
gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg	720

```

ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc 780
gactgcagcc acgccccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc 900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt 960
gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggc 1020
gtgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctggtcga gctggacggc 1080
gacgtaaacy gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 1140
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gccaccctc 1200
gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgtac catcttcttc 1320
aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg 1380
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 1440
ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc 1500
atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 1620
ctgagcaccc agtcgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680
ctggagtctg tgaccgccgc cgggatcact ctggcgatgg acgagctgta caaggctgag 1740
gctgcagcgc gcgaagcatg ctgcccaggt tgttgcgctc gcgcatga 1788

```

<210> 44

<211> 595

<212> PRT

<213> artificial sequence

<220>

<223> A2A-CFP-ModelPG-C49 amino acid sequence

<400> 44

```

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1           5           10          15

```

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr

	245		250		255
Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu	260		265		270
Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr	275		280		285
Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg	290		295		300
Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser	305		310		315
Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu	325		330		335
Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val	340		345		350
Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser	355		360		365
Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu	370		375		380
Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu	385		390		395
Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp	405		410		415
His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr	420		425		430
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr	435		440		445
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu	450		455		460
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys	465		470		475
					480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
565 570 575

Tyr Lys Ala Glu Ala Ala Ala Arg Glu Ala Cys Cys Pro Gly Cys Cys
580 585 590

Ala Arg Ala
595

<210> 45

<211> 1737

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP-C49 cDNA sequence

<400> 45
atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc 120
accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 180
ccctttgccca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240

gcctgcttcg	tcctggctct	cacgcagagc	tccatcttca	gtctcctggc	catcgccatt	300
gaccgctaca	ttgccatccg	catcccgcctc	cggtacaatg	gcttggtgac	cggcacgagg	360
gctaagggca	tcattgccat	ctgctgggtg	ctgtcgtttg	ccatcggcct	gactcccatg	420
ctaggttgga	acaactgcgg	tcagccaaag	gagggcaaga	accactccca	gggctgcggg	480
gagggccaag	tggcctgtct	ctttgaggat	gtggtcccca	tgaactacat	ggtgtacttc	540
aacttctttg	cctgtgtgct	ggtgcccctg	ctgctcatgc	tgggtgtcta	tttgcggatc	600
ttcctggcgg	cgcgacgaca	gctgaagcag	atggagagcc	agcctctgcc	gggggagcgg	660
gcacggtcca	cactgcagaa	ggaggtccat	gctgccaagt	cactggccat	cattgtgggg	720
ctctttgccc	tctgctggct	gcccctacac	atcatcaact	gcttcacttt	cttctgcccc	780
gactgcagcc	acgcccctct	ctggctcatg	tacctggcca	tcgtcctctc	ccacaccaat	840
tcggttggtga	atcccttcat	ctacgcctac	cgtatccgcg	agttccgcca	gaccttccgc	900
aagatcattc	gcagccacgt	cctgaggcag	caagaacctt	tcaaggcagc	tggcaccagt	960
gcccgggtct	tggcagctca	tggcagtgac	ggagagcagg	tcagcctccg	tctcaacggt	1020
gtgagcaagg	gcgaggagct	gttcaccggg	gtggtgcccc	tcctggtcga	gctggacggc	1080
gacgtaaacy	gccacagggt	cagcgtgtcc	ggcgagggcg	agggcgatgc	cacctacggc	1140
aagctgaccc	tgaagttcat	ctgcaccacc	ggcaagctgc	ccgtgccttg	gcccaccctc	1200
gtgaccaccc	tgacctgggg	cgtgcagtgc	ttcagccgct	accccgacca	catgaagcag	1260
cacgacttct	tcaagtccgc	catgcccga	ggctacgtcc	aggagcgtac	catcttcttc	1320
aaggacgacg	gcaactacaa	gacccgcgcc	gaggtgaagt	tcgagggcga	caccttggtg	1380
aaccgcatcg	agctgaaggg	catcgacttc	aaggaggacg	gcaacatcct	ggggcacaag	1440
ctggagtaca	actacatcag	ccacaacgtc	tatatcaccg	ccgacaagca	gaagaacggc	1500
atcaaggccc	acttcaagat	ccgccacaac	atcgaggacg	gcagcgtgca	gctcgccgac	1560
cactaccagc	agaacacccc	catcggcgac	ggccccgtgc	tgctgcccga	caaccactac	1620
ctgagcacc	agtccgcct	gagcaaagac	cccaacgaga	agcgcgatca	catggtcctg	1680
ctggagttcg	tgaccgccgc	cgggatcact	ctcggcatgg	acgagctgta	caagtaa	1737

<210> 46

<211> 578

<212> PRT

<213> artificial sequence

<220>

<223> A2A-CFP-C49 amino acid sequence

<400> 46

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
565 570 575

Tyr Lys

50/66

51/66